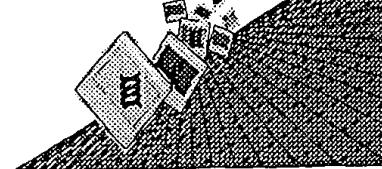
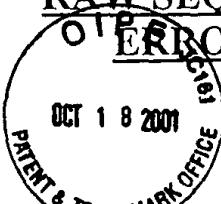


Sorbelli

BIO1, JHN, CGY
SYSTEMS
BRANCH

7-26-0
PZ

RAW SEQUENCE LISTING
OF
ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/515, 369A

RECEIVED

Source: 1633

JUL 25 2001

Date Processed by STIC: 7-5-01

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



RECEIVED

JUL 25 2001

Sequence Listing Error Summary

TECH CENTER 1600/2900

ERROR DETECTEDSUGGESTED CORRECTIONSERIAL NUMBER: 09/515,369A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic Acids The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.



1633

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/515,369A

DATE: 07/05/2001
TIME: 12:54:49

Input Set : A:\56778.txt
Output Set: N:\CRF3\07032001\I515369A.raw

3 <110> APPLICANT: Fisher, Paul
4 Madireddi, Malavi
6 <120> TITLE OF INVENTION: MELANOMA DIFFERENTIATION ASSOCIATED GENE-7 PROMOTER AND USES
THEREOF

8 <130> FILE REFERENCE: 0575/56778/JPW/APE
10 <140> CURRENT APPLICATION NUMBER: 09/515,369A
11 <141> CURRENT FILING DATE: 2000-02-29
13 <160> NUMBER OF SEQ ID NOS: 13
15 <170> SOFTWARE: PatentIn version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 2286
19 <212> TYPE: DNA
20 <213> ORGANISM: Human
22 <400> SEQUENCE: 1

23	taatacgaact cactataggg cgtcgactcg atcacctttt gaaccagggt ctgcctgcct	60
25	ccaaagcttg tactcataac tagattctca actgatgttg ggccaagggtt cctagttct	120
27	ctccttgcacc ttcccttctga agtaataatg ctatgataag ctcatcgagg gctgaggccc	180
29	aggcacatgt ttgcctgaac tatccatgtt atatgattcc ttccctcagac agagttagct	240
31	actcacatgc ccagggtgtac cctgaggcca gccaagggtgt atccatgacc tcattgcctct	300
33	gttccagcct gcccttaac agtcataccc acctgcctgc cctcccccgc tatctgcaga	360
35	cagtagtcta ggatttcaga tgccctgggg gtcattttc cctctcagct tcctgcctta	420
37	gctgtctcct gcctccact cacattttac tccagactc tcacctggc ttctttctg	480
39	tctcatcact gcctcttgac atcttatct catagtagtt agtttaggggt tcttggtaat	540
41	gcctctaaatc cacatgggtt ggaggggggg gtggggggaa agagtgcgt gtggggctgt	600
43	gcctactttt ggagggttaag actcgggccc tccaggaaca aaggattcag gctgggtggca	660
45	gctatagcca agcagactgc tggccaggga ttgcaaagga gtattttgt tgcttaagaa	720
47	aataaacaac actgagatgtt agatggaggg agggtttgtt ggtgccagag agattggaa	780
49	gagtctgcca aggggtgtttt ctactcactc tcctttttc ttcatctcc actgagctgg	840
51	aggcaggttat cctgtcccc acgtcacatt cctactccc ttcccatgc ctggacccag	900
53	gttgggcaaa ctcttcctgt aaagaaccag acaggaacta ttttaggctc tgtgtgccat	960
55	atgggtctcag tcacaactac tcatctctgc ctctgttagca cgaaagcaat tagcaacaat	1020
57	atgtcaacaa acatatgtga ccccatgaaa actttatata ttatggatac ggaaacctga	1080
59	aaataaatgtc ttcttttga tttttttccc aatcattaaa aaacgtaaaaa actactctta	1140
61	ggtcgcaagg ttaagccatt ctcaagttttag cagtggcagg ctggattttgg cttgtgacct	1200
63	acagttggcc aatccctgtat tcccaaaatg tattcctcag ggtatgtggc aaataacttat	1260
65	ggaaagtgtt ggattaaaca gagttaaagaa gcatcagaca ttccaggac gggctagcac	1320
67	atgccaggc tctctactg acctcattgg attcatctgt ttcatggagg atcttgcaag	1380
69	acaagaattc ctcaaaccata gagtctgagg actgtgtttt gggaaacact gctctgcttg	1440
71	atgccctcac tggcacatg gtataatcta gagctgagtg cttctgttagc tggagatagg	1500
73	gtcagagctc ttgactgccc tggcagtctt gacacatcac gctgtctgtg tccctgtagt	1560
75	ggttcagagc cacacaggcc aagactagcc caccagagca ccaggcctcc cagctttctg	1620
77	ggcttgcata tccttattct tcctggttc cagaacctaa ggagaggcac	1680
79	atttgggtt agtattttt accctaggaa ccatgggttag ctgcattgtca ggaaacactc	1740
81	ctcaacttcc tggccctgtat ggattaaagg agaggtactt acaggttatt ttctcgctgt	1800
83	ggactactgt cccagcatga atagggcattt attattttat tattttgaca ggaaggagac	1860
85	tgggttatgc tgcacagtaa taatgtattt acatgtgtac agagtttacc aagcacctct	1920
87	gtgttggttt tgcctttgtt tattacactt gggacaaatt tttaaaattt atacatgcag	1980
89	agactgcagc gcagagaagc taagagactt gccctgcctt acacagccag tggtagagcc	2040

Does Not Comply
Corrected Diskette Needed

See p. 4

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/515,369A

DATE: 07/05/2001
TIME: 12:54:49

Input Set : A:\56778.txt
Output Set: N:\CRF3\07032001\I515369A.raw

91 tgaactcaa cccaggtctc atctcaccc aggggctgct ttccccatcg ctgtattgtc 2100
93 cttaaaagtga tgggtgacta ggcaatgaag taattctcta gaaaaagcatg accaatttcc 2160
95 ctttctccac ctccctctt ttccctccacc cctccccat cagccccat atatatgcc 2220
97 aaatctccac aaagccttgc ttgcctgcaa accttactt ctgaaaatgac ttccacggct 2280
99 gggacg 2286
102 <210> SEQ ID NO: 2
103 <211> LENGTH: 21
104 <212> TYPE: DNA
105 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <221> NAME/KEY: misc_feature
109 <222> LOCATION: ()..()
110 <223> OTHER INFORMATION: primer
113 <400> SEQUENCE: 2
114 cgtcccagcc gtggaaagtca t 21
117 <210> SEQ ID NO: 3
118 <211> LENGTH: 21
119 <212> TYPE: DNA
120 <213> ORGANISM: Artificial Sequence
122 <220> FEATURE:
123 <221> NAME/KEY: misc_feature
124 <222> LOCATION: ()..()
125 <223> OTHER INFORMATION: primer
128 <400> SEQUENCE: 3
129 aggctggatt tggcttgtga c 21
132 <210> SEQ ID NO: 4
133 <211> LENGTH: 21
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:
138 <221> NAME/KEY: misc_feature
139 <222> LOCATION: ()..()
140 <223> OTHER INFORMATION: primer
143 <400> SEQUENCE: 4
144 ctgtttaatc cagcacttcc c 21
147 <210> SEQ ID NO: 5
148 <211> LENGTH: 21
149 <212> TYPE: DNA
150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <221> NAME/KEY: misc_feature
154 <222> LOCATION: ()..()
155 <223> OTHER INFORMATION: primer
158 <400> SEQUENCE: 5
159 cgcttgatga ctcagccgga a 21
162 <210> SEQ ID NO: 6
163 <211> LENGTH: 20
164 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/515,369A

DATE: 07/05/2001

TIME: 12:54:49

Input Set : A:\56778.txt

Output Set: N:\CRF3\07032001\I515369A.raw

167 <220> FEATURE:
168 <221> NAME/KEY: misc_feature
169 <222> LOCATION: ()..()
170 <223> OTHER INFORMATION: primer
173 <400> SEQUENCE: 6
174 tgcagattgc gcaatctgca 20
177 <210> SEQ ID NO: 7
178 <211> LENGTH: 21
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <221> NAME/KEY: misc_feature
184 <222> LOCATION: ()..()
185 <223> OTHER INFORMATION: primer
188 <400> SEQUENCE: 7
189 cgcttgatga cttggccgga a 21
192 <210> SEQ ID NO: 8
193 <211> LENGTH: 22
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <221> NAME/KEY: misc_feature
199 <222> LOCATION: ()..()
200 <223> OTHER INFORMATION: primer
203 <400> SEQUENCE: 8
204 tgcagagaga ctatgtcttg ca 22
207 <210> SEQ ID NO: 9
208 <211> LENGTH: 61
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <221> NAME/KEY: misc_feature
214 <222> LOCATION: ()..()
215 <223> OTHER INFORMATION: primer
218 <400> SEQUENCE: 9
219 uuguauuuau uacaacucua uuuuauuuau gucaguauuu caacugaagu ucuauuuauu 60
221 u 61
224 <210> SEQ ID NO: 10
225 <211> LENGTH: 15
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <221> NAME/KEY: misc_feature
231 <222> LOCATION: ()..()
232 <223> OTHER INFORMATION: primer
235 <400> SEQUENCE: 10
236 uauuuauuuua uuuuaa 15
239 <210> SEQ ID NO: 11
240 <211> LENGTH: 51

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/515,369A

DATE: 07/05/2001
TIME: 12:54:49

Input Set : A:\56778.txt
Output Set: N:\CRF3\07032001\I515369A.raw

241 <212> TYPE: DNA		
242 <213> ORGANISM: Artificial Sequence		
244 <220> FEATURE:		
245 <221> NAME/KEY: misc_feature		
246 <222> LOCATION: ()..()		
247 <223> OTHER INFORMATION: primer		
250 <400> SEQUENCE: 11		
251 uaaaaauuuau auauuuauau uuuuaaaaua uuuauuuauu uauuuauuuua a		51
254 <210> SEQ ID NO: 12		
255 <211> LENGTH: 38		
256 <212> TYPE: DNA		
257 <213> ORGANISM: Artificial Sequence		
259 <220> FEATURE:		
260 <221> NAME/KEY: misc_feature		
261 <222> LOCATION: ()..()		
262 <223> OTHER INFORMATION: primer		
265 <400> SEQUENCE: 12		
W--> 266 suncauuuau uauuuuuau uuaauuuuaa uuuauuuua		38
269 <210> SEQ ID NO: 13		
270 <211> LENGTH: 56		
271 <212> TYPE: DNA		
272 <213> ORGANISM: Artificial Sequence		
274 <220> FEATURE:		
275 <221> NAME/KEY: misc_feature		
276 <222> LOCATION: ()..()		
277 <223> OTHER INFORMATION: primer		
280 <400> SEQUENCE: 13		
281 guuuuuuauu uauuuuuaua gauggauucu cagauuuua uauuuuuauu uuaauu		56

Sequence #12 is missing the mandatory <220> to <223> features to explain the "n" in the sequence See #9 on the Error Summary Sheet.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/515,369A

DATE: 07/05/2001
TIME: 12:54:50

Input Set : A:\56778.txt
Output Set: N:\CRF3\07032001\I515369A.raw

L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12